to expedite the prosecution of the application. Applicants reserve the right to pursue the claims as originally filed in this or a separate application(s).

Objection to the Specification

The Examiner has objected to the specification because it, "contains black spaces in several pages."

Applicants respectfully submit that, pursuant to *In re Lundak*, Applicants have the right to make a deposit of a plasmid containing a nucleotide sequence of the molecules of the present invention, prior to issuance of the application. *In re Lundak* 723 F2.d 1216, 227 USPQ 90 (Fed. Cir. 1985). Accordingly, Applicants reserve the right to amend the specification as originally filed to include the ATCC Deposit information for these molecules when this information becomes available and prior to issuance of the application.

Objection to the Claims

The Examiner has objected to claims 37 and 41 because they, "recite an abbreviation."

Applicants have amended claims 37 and 41 such that they no longer contain an abbreviation. Accordingly, Applicants respectfully request that the Examiner reconsider and withdraw this objection.

Rejection of Claims 32, 33, 38, 39, 42, and 46 Under 35 U.S.C. § 112, Second Paragraph

The Examiner has rejected claims 32, 33, 38, 39, 42, and 46 under 35 U.S.C. § 112, second paragraph as being, "incomplete for omitting essential steps, such omission amounting to a gap between the steps." The Examiner further states that the omitted steps are, "the method of determining whether the polypeptide has bound to the test compound."

Applicants respectfully traverse the foregoing rejection on the grounds that the claims are clear and definite in view of the teachings in Applicants' specification. Applicants' claims are directed to a method for identifying a compound that binds to a polypeptide of the invention. The method includes contacting the polypeptide or a cell

containing the polypeptide with a test compound under conditions suitable for binding to the polypeptide and determining whether the polypeptide binds to the test compound. Applicants have disclosed numerous ways in which this binding may be tested. For Example, Applicants teach at page 50, line 34 through page 55, line 13 of the specification numerous *in vivo* and *in vitro* methods which may be used to determine if a test compound is capable of binding to the polypeptide of the instant invention. Since the pending claims set out the steps necessary to determine test compound binding to the polypeptide of the instant invention, Applicants should not be limited to anyone specific way of determining the ability of a test compound to bind to the polypeptides of the invention.

In view of the foregoing teachings in Applicants' specification the ordinary skilled artisan would find the pending claims to be clear and definite. Accordingly, Applicants respectfully request that the Examiner reconsider and withdraw this rejection.

Rejection of Claims 42-45 Under 35 U.S.C. § 112, First Paragraph

The Examiner has rejected claims 42-45 under 35 U.S.C. § 112, first paragraph because, according to the Examiner, "the specification, while being enabling for a method of identifying a compound which binds to a polypeptide comprising the amino acid sequence SEQ ID NO:2, does not reasonably provide enablement for a method of identifying a compound which binds to a polypeptide comprising any contiguous 10 amino acids." In particular, the Examiner is of the opinion that

> [t]he specification does not support the broad scope of the claims which encompass all modifications and fragments of any HGT which matches only to any 10 contiguous amino acids with SEQ ID NO:2 because the specification does not establish: (A) regions of the protein structure which may be modified without effecting HGT activity; (B) the general tolerance of human HGT's to modification and extent of such tolerance; (C) a rational and predictable scheme for modifying any human GFT amino acid residues with an expectation of obtaining the desired biological function; and (D) the specification provides insufficient guidance as to which of the essentially infinite possible choices is likely to be successful.
> Thus, applicants have not provided sufficient guidance to enable one of ordinary skill in the art to make and use the claimed invention in a manner reasonably correlated with the scope of the claims broadly including al or

any human HGT with an enormous number of amino acid modifications of SEQ ID NO:2.

Applicants traverse the foregoing rejection for the following reasons.

Applicants respectfully submit that the specification provides ample information regarding the structure/function relationship of the galactosyltransferase molecules, *e.g.*, HGT-1 molecules of the present invention. To begin with, Applicants' specification discloses at, for example, page 2, lines 9-20, that the HGT-1 molecule of the invention is a galactosyltransferase, having at least one conserved galactosyltransferase domain. Moreover, Applicants' specification discloses that the HGT-1 polypeptide of the invention is a membrane bound polypeptide with at least one transmembrane domain. Applicants' specification also teaches that the aforementioned conserved domains and amino acid residues are essential for the functional activity of the HGT-1 polypeptide, and thus, that these domains and the residues that comprise these domains, are not likely to be amenable to alteration. Further, Applicants provide, in Figures 3 and 4, the location of the domains, *e.g.*, transmembrane domains and a galactosyltransferase family domain, that are necessary to the HGT-1 activity. Accordingly, Applicants respectfully submit that an ordinarily skilled artisan reading Applicants' specification would have know which residues can be altered without affecting the functional activity of the HGT-1 polypeptide.

Moreover, Applicants' specification describes extensively how to make and use fragments of the claimed polypeptide sequences. For example, at page 26, line 16, through page 27, line 6, and at page 31, lines 4-27 of the specification, Applicants disclose various length fragments of the claimed polypeptides, as well as their use as immunogens and as targets for developing agents that modulate HGT-1 activity. Further, at page 50, line 1, through page 57, line 25 of the specification Applicants disclose how to use such fragments in, for example, screening assays.

In addition, Applicants respectfully submit that the present specification teaches (and is also well known in the art) how to generate fragments of a polypeptide. Such fragments may be prepared by standard techniques, *e.g.*, by using a DNA fragment in an expression vector or they may be generated by the use of enzymes that cleave at specific sites within the polypeptide.

With respect to the new claims directed to methods which use polypeptides that are at least 95% identical to SEQ ID NO:2 and retain a human galactosyltransferase activity, Applicants would like to bring to the Examiner's attention Example 14 of the *Revised Interim Written Description Guidelines Training Materials*. This example provides that a claim directed to variants of a protein having SEQ ID NO:3 "that are at least 95% identical to SEQ ID NO:3 and catalyze the reaction of A→B" with an accompanying specification that discloses a single species falling within the claimed genus, satisfies the requirements of 35 U.S.C. §112, first paragraph for written description. The rationale behind the foregoing conclusion, as presented by the *Written Description Guidelines*, is that "[t]he single species disclosed is representative of the genus because all members have at least 95% structural identity with the reference compound and because of the presence of an assay which Applicant provided for identifying all of the at least 95% identical variants of SEQ ID NO:3 which are capable of the specified catalytic activity." The Guidelines also provide that "***[t]he procedures for making variants of SEQ ID NO:3 are conventional in the art and an assay is described which will identify other proteins having the claimed catalytic activity. Moreover, procedures for making variants of SEQ ID NO:3 which have 95% identity to SEQ ID NO:3 and retain its activity are conventional in the art***."

Similarly, in the present case, the newly added claims are directed to methods which use polypeptides comprising an amino acid sequence that is at least 95% identical to the amino acid sequence shown in SEQ ID NO:2, wherein the polypeptide retains a galactosyltransferase activity. As set forth in Example 14 of the Written Description Guidelines, the production of polypeptides which contain a 5% variation from a specific sequence is routine in the art. Furthermore, Applicants have disclosed in the instant specification assays for identifying all of the at least 95% identical variants of SEQ ID NO:2 that retain a galactosyltransferase activity (see, for example, page 50, line 34 through page 55, line 13 of the specification).

In view of the foregoing, Applicants respectfully submit that an ordinarily skilled artisan following the teachings provided by Applicants' specification would have been able to practice the claimed invention using only routine experimentation. Accordingly,

the aforementioned rejection of the pending claims under section 112, first paragraph, is improper, and Applicants respectfully request that the Examiner reconsider and withdraw this rejection.

Rejection of Claims 42-45 Under 35 U.S.C. § 112

The Examiner has rejected claims 42-45 under 35 U.S.C. § 112, first paragraph, as, "containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the art that the inventors, at the time the application was filed, had possession of the claimed invention." The Examiner is of the opinion that these claims "are directed to a method of using a genus of polypeptide fragments of SEQ ID NO:2 that have not been disclosed in the specification."

Applicants traverse the foregoing rejection. Applicants submit that there is sufficient written description in Applicants' specification regarding the claimed invention, to inform a skilled artisan that Applicants were in possession of the claimed invention at the time the application was filed, as required by §112, first paragraph (see M.P.E.P. 2163.02). "Written description may be satisfied through disclosure of relevant identifying characteristics, *i.e.*, structure, other physical and/or chemical characteristics, functional characteristics when coupled with a known or disclosed correlation between function and structure, or some combination of such characteristics." *Interim Guidelines for Examination of Patent Applications Under the 35 U.S.C. §112, First Paragraph Written Description Requirement*. Moreover, "[a] specification may, within the meaning of 35 U.S.C. §112, First paragraph, contain a written description of a broadly written claimed invention ***without describing all species that claim encompasses***." *Utter v. Hiraga*, 845 F.2d 993, 6 USPQ2d 1709 (Fed. Cir. 1988). Moreover, the *In re Grimme* case sets out the following language with respect to the written description requirement, "[i]t may not be necessary to enumerate a plurality of species if a genus is sufficiently identified in an application by 'other appropriate language.'" *In re Grimme*, 274 F.2d 949, 952, 124 USPQ 499, 501 (CCPA 1960).

For reasons discussed in detail below, the instant specification satisfies this requirement for the claimed invention. It is Applicants' position that the genus of polypeptide molecules of the present invention is defined by structural features that are described in the specification and commonly possessed by its members. Contrary to the

Examiner's assertion, Applicants respectfully submit that the instant specification teaches distinguishing structural features within the foregoing genus. In particular, Applicants' specification teaches that the galactoysltransferase-1 polypeptides of the present invention contain a conserved transmembrane domain and a galactosyltransferase family domain (see, *e.g.*, page 9, line 7 through page 10, line 18, and Figures 3 and 4). Thus, Applicants' specification teaches which regions of the polypeptide molecules of the invention are essential for activity and which are not, and, thus, which regions of the polypeptides of the invention are amenable to alteration and which are not.

In Example 15 of the *Interim Guidelines for Examination of Patent Applications Under the 35 U.S.C. §112, First Paragraph Written Description Requirement* the "theoretical specification" discloses a messenger RNA sequence, SEQ ID NO:1, which encodes a human growth hormone. The "theoretical specification" claims antisense molecules that inhibit the production of human growth hormone. The Guidelines provide that

> [c]onsidering the specification's disclosure of (1) ***the sequence (SEQ ID NO:1) which defines and limits the structure of any effective molecules such that one skilled in the art would be able to immediately envisage members of the genus embraced by the claim*** and 2) the functional characteristics of the claimed invention as well as a routine art-recognized method of screening for antisense molecules which provide further distinguishing characteristics of the claimed invention, along with, 3) the general level of knowledge and skill in the art, one skilled in the art would conclude that applicant was in possession of the invention.....***the claimed invention is adequately described. (Emphasis added).***

Similar to Example 15 of the *Interim Guidelines*, the instant specification describes the amino acid sequence of the polypeptides of the invention (SEQ ID NO:2) ***which define and limit the structure of any polypeptide fragments such that one skilled in the art would be able to immediately envisage members of the genus embraced by the polypeptide fragment claims***.

Moreover, as provided in Example 15 of the *Interim Guidelines*, the generation of polypeptide fragments (like the generation of oligonucleotide fragments) is routine. For example, (as indicated in Example 15 of the *Interim Guidelines*) any specified fragment

can be ordered from a commercial synthesizing service. Finally, Applicants' specification teaches how such polypeptide fragments may be used in the claimed screening assays (see, for example, page 50, line 34 through page 55, line 13 of the specification).

With respect to the new claims directed to methods which use polypeptides that are at least 95% identical to SEQ ID NO:2 and retain a human galactosyltransferase activity, Applicants would like to bring to the Examiner's attention Example 14 of the *Revised Interim Written Description Guidelines Training Materials*. This example provides that ***a claim directed to variants of a protein having SEQ ID NO:3 "that are at least 95% identical to SEQ ID NO:3 and catalyze the reaction of A→B" with an accompanying specification that discloses a single species falling within the claimed genus, satisfies the requirements of 35 U.S.C. §112, first paragraph for written description.*** The rationale behind the foregoing conclusion, as presented by the *Written Description Guidelines*, is that "[t]he single species disclosed is representative of the genus because all members have at least 95% structural identity with the reference compound and because of the presence of an assay which Applicant provided for identifying all of the at least 95% identical variants of SEQ ID NO:3 which are capable of the specified catalytic activity." The Guidelines also provide that "[t]he procedures for making variants of SEQ ID NO:3 are conventional in the art and an assay is described which will identify other proteins having the claimed catalytic activity. Moreover, procedures for making variants of SEQ ID NO:3 which have 95% identity to SEQ ID NO:3 and retain its activity are conventional in the art."

Similarly, in the present case, the newly added claims are directed to methods which use polypeptides comprising an amino acid sequence that is at least 95% identical to the amino acid sequence shown in SEQ ID NO:2, wherein the polypeptide retains a galactosyltransferase activity. Applicants have disclosed in the instant specification assays for identifying all of the at least 95% identical variants of SEQ ID NO:2 that retain a galactosyltransferase activity (see, for example, page 50, line 34 through page 55, line 13 of the specification).

Based on the above teachings, an ordinary skilled artisan would have recognized that Applicants were in possession of the claimed invention at the time the application was filed. Accordingly, Applicants respectfully request that the Examiner reconsider and withdraw the foregoing rejection.

Rejection of Claims 46-48 Under 35 U.S.C. § 112

The Examiner has rejected claims 46-48 under 35 U.S.C. § 112 as, "containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventors, at the time the application was filed had possession of the claimed invention."

Without acquiescing to the Examiner's rejection and solely in the interest of expediting prosecution, Applicants have cancelled claims 46-48 thereby rendering this rejection moot. Accordingly, Applicants respectfully request that the Examiner reconsider and withdraw this rejection.

Rejection of Claims 46-48 Under 35 U.S.C. § 103

The Examiner has rejected claims 46-48 under 35 U.S.C. § 103 as being unpatentable over Phillerr *et al.*, or Isshiki *et al.*, or Amado *et a*l., or Conklin *et al.*

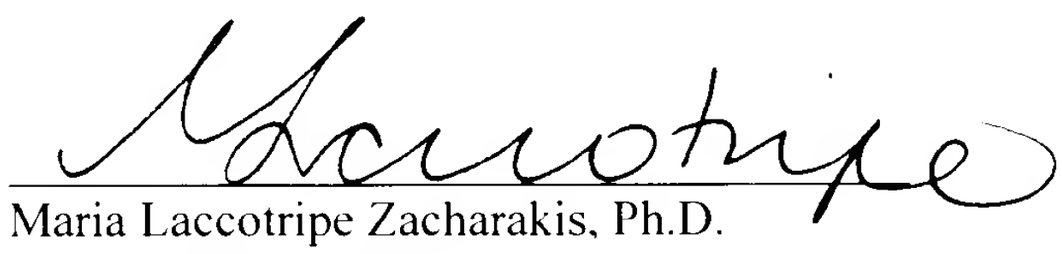
Without acquiescing to the Examiner's rejection and solely in the interest of expediting prosecution, Applicants have cancelled claims 46-48 thereby rendering the foregoing rejection moot. Accordingly, Applicants request that the Examiner reconsider and withdraw this rejection.

CONCLUSION

In view of the amendments and remarks set forth above, it is respectfully submitted that this application is in condition for allowance. If there are any remaining issues or the Examiner believes that a telephone conversation with Applicants' Attorney would be helpful in expediting prosecution of this application, the Examiner is invited to call the undersigned at (617) 227-7400.

Respectfully submitted,

LAHIVE & COCKFIELD, LLP



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Date: **January 22, 2003**

VERSION WITH MARKINGS TO SHOW CHANGES MADE

37. The method of claim 32, wherein said binding of the polypeptide is detected by use of an assay for ~~HGT-1~~ human galactosyltransferase-1 activity.

41. The method of claim 38 or 39, wherein said binding of the polypeptide is detected by use of an assay for ~~HGT-1~~ human galactosyltransferase-1 activity.

APPENDIX A

32. A method for identifying a compound which binds to a polypeptide comprising the amino acid sequence of SEQ ID NO:2, the method comprising:

a) contacting a cell expressing the polypeptide with a test compound under conditions suitable for binding to the polypeptide; and

b) determining whether the polypeptide binds to the test compound.

33. A method for identifying a compound which binds to a polypeptide consisting of the amino acid sequence of SEQ ID NO:2, the method comprising:

a) contacting a cell expressing the polypeptide with a test compound under conditions suitable for binding to the polypeptide; and

b) determining whether the polypeptide binds to the test compound.

34. The method of claim 32 or 33, wherein said binding of the polypeptide is detected by direct binding of the test compound to the polypeptide.

35. The method of claim 34, wherein said direct binding is determined by lysing the cell and performing an immunoprecipitation.

36. The method of claim 34, wherein said direct binding is determined by a yeast two-hybrid assay.

37. The method of claim 32, wherein said binding of the polypeptide is detected by use of an assay for human galactosyltransferase-1 activity.

38. A method for identifying a compound which binds to a polypeptide comprising the amino acid sequence of SEQ ID NO:2, the method comprising:

a) contacting the polypeptide with a test compound under conditions suitable for binding to the polypeptide; and

b) determining whether the polypeptide binds to the test compound.

39. A method for identifying a compound which binds to a polypeptide consisting of the amino acid sequence of SEQ ID NO:2, the method comprising:

a) contacting the polypeptide with a test compound under conditions suitable for binding to the polypeptide; and

b) determining whether the polypeptide binds to the test compound.

40. The method of claim 38 or 39, wherein said binding of the polypeptide is detected by the use of a competition binding assay.

41. The method of claim 38 or 39, wherein said binding of the polypeptide is detected by use of an assay for human galactosyltransferase-1 activity.

42. A method for identifying a compound which binds to a polypeptide comprising at least 10 contiguous amino acids of SEQ ID NO:2, the method comprising:

a) contacting the polypeptide with a test compound under conditions suitable for binding of the polypeptide; and

b) determining whether the polypeptide binds to the test compound.

43. The method of claim 42, wherein said binding of the polypeptide is detected by direct binding of the test compound to the polypeptide.

44. The method of claim 43, wherein said direct binding is determined by an immunoprecipitation.

45. The method of claim 42, wherein said binding of the polypeptide is detected by the use of a competition binding assay.

49. A method for identifying a compound which binds to a polypeptide comprising the amino acid sequence of SEQ ID NO:2, the method comprising:

a) contacting a cell expressing said polypeptide with a test compound under conditions suitable for binding to said polypeptide; and

b) determining whether said polypeptide binds to said test compound by detecting a labeled polypeptide or a labeled test compound in a complex.

50. A method for identifying a compound which binds to a polypeptide comprising an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:2 and retains a human galactosyltransferase-1 activity, the method comprising:

a) contacting a cell expressing said polypeptide with a test compound under conditions suitable for binding to said polypeptide; and

b) determining whether said polypeptide binds to said test compound by detecting a labeled polypeptide or a labeled test compound in a complex.

51. A method for identifying a compound which binds to a polypeptide comprising the amino acid sequence of SEQ ID NO:2, the method comprising:

a) contacting said polypeptide with a test compound under conditions suitable for binding to said polypeptide; and

b) determining whether said polypeptide binds to said test compound by detecting a labeled polypeptide or a labeled test compound in a complex.

52. A method for identifying a compound which binds to a polypeptide comprising an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:2 and retains a human galactosyltransferase-1 activity, the method comprising:

a) contacting said polypeptide with a test compound under conditions suitable for binding to said polypeptide; and

b) determining whether said polypeptide binds to said test compound by detecting a labeled polypeptide or a labeled test compound in a complex.

53. A method for identifying a compound which binds to a polypeptide comprising the amino acid sequence of SEQ ID NO:2, the method comprising:

a) contacting a cell expressing said polypeptide with a test compound under conditions suitable for binding to said polypeptide;

b) detecting the activity of said polypeptide in the presence and in the absence of said compound; and

c) determining whether said polypeptide binds to said test compound by detecting a modulation in the activity of said polypeptide in the presence of said compound.

54. A method for identifying a compound which binds to a polypeptide comprising an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:2 and retains a human galactosyltransferase-1 activity, the method comprising:

a) contacting a cell expressing said polypeptide with a test compound under conditions suitable for binding to said polypeptide;

b) detecting the activity of said polypeptide in the presence and in the absence of said compound; and

c) determining whether said polypeptide binds to said test compound by detecting a modulation in the activity of said polypeptide in the presence of said compound.

55. A method for identifying a compound which binds to a polypeptide comprising the amino acid sequence of SEQ ID NO:2, the method comprising:

a) contacting said polypeptide with a test compound under conditions suitable for binding to said polypeptide;

b) detecting the activity of said polypeptide in the presence and in the absence of said compound; and

c) determining whether said polypeptide binds to said test compound by detecting a modulation in the activity of said polypeptide in the presence of said compound.

56. A method for identifying a compound which binds to a polypeptide comprising an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:2 and retains a human galactosyltransferase-1 activity, the method comprising:

a) contacting said polypeptide with a test compound under conditions suitable for binding to said polypeptide;

b) detecting the activity of said polypeptide in the presence and in the absence of said compound; and

c) determining whether said polypeptide binds to said test compound by detecting a modulation in the activity of said polypeptide in the presence of said compound.